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ACACTGGANG AAGGGCGCAC CCTGGCAGAT TNCNACATT C NAAAGAATC CACCTTCACC	600
TGGTGCTCCC CCTCCGCCGG GGTCCCTAAC CCTTTTGGGC TGTATGTNTC CCCTGCCTTT	660
5 GCTGTCTTAA TTCNCTCTGT TGGTGGTGT TGGAAATTCC CTAATCCNGA AGGTTCTTNA	720
AAAGGAAATN AANCCNNNTG GGTTTCCCCC TTTGGCCTTT TTTTTGTTG AAAATCCTNT	780
10 GTTTTGGTG T	791

10 (2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 814 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

20 (ii) MOLECULE TYPE: cDNA

25 (vii) IMMEDIATE SOURCE:

- (B) CLONE: U-U120

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

GGCACNANCC CGCTTCGGTA GCCATTATTG GTGCCCGTAG AGCGAGTGCT GAGATGGCTT	60
TGAGGGCCTT CTTCCCCCTC TGCACTCGCTC TCGTGGTGAC GCTCTCACCT CTGTGTGATG	120
CCACTTCGCC TTACTACACC ATCACACCGC CCACCCCCGT GGCCAAGCCG CCTTCAGTTG	180
AACCACCACC CTACCACGGC CCTCCGACNA CCCACCCCTAA GCCACCGAGT CATGGTGGCC	240
AACCTCCGTC CCACCACATCAC CCAACACCAA TCTACGGTGC ACCCCCTCCG CAACACCACC	300
ACCACCAACCA ACACCACAC CAACCTGCAC CACCAACTCA CGCANAACAC CCTCCGTACT	360
ACCACATGCC TTCCCCGCCG CCGCATGGCC AGCACCCGTC ACCACCGTCA CATGATTATC	420
CCGTACCTCC TGCTCACAAG CCCCCGAACTC CGCCGCCGGT TTACAAGTCT CCACCCACCGA	480
45 NCCACCGTCC TTACCCCTCCA TCGACGCCAC CCCACCATCC GAAGCACCCG CCTTCAGC	540
CGAAGCCGTC NTACAAGGCC CGCCACCATN CAAGAACATC CCTGANCACT CTCCACCGCC	600
GGTCACTAT CATTCTCCGT CTTCACCAACC ACCACCAACCA CCATACAAAAA TAATCTCGTT	660
50 TTGCCATCTT CTCCCGTTTG AAAAAAANN CAANTGTCT TTTTATTAA CCNAATCCAN	720
GGGGTTTTTN TTAANATTNN AANAAANCNA ANTNTTTCC CCCCCNTNTT GGTTNATGGC	780
55 CTATGGGTTT GTTTCTCTTC TTGGCTTTTC CCGG	814

55 (2) INFORMATION FOR SEQ ID NO: 30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 742 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

65 (ii) MOLECULE TYPE: cDNA

70 (vii) IMMEDIATE SOURCE:

- (B) CLONE: U-U126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

5	GGCACGAGGT TGTGCCAAC AGAGAGAGAG AGAGACAGAC CGATAGCCTC CTCATTCACT	60
	ATGGCGATCC GATGCCAGC TTGCGCTGCTG TTATTTGCCT TTCTGATGCT TGCGCTCACA	120
	GGAAGACTGC AGGCCGGGCG CAGCTCATGC ATTGGCGTCT ACTGGGGACA AAACACAGAC	180
10	GAGGGAAGCT TAGCAGATGC TTGTGCCACA GGCAACTACG AATACGTGAA CATGCCACC	240
	CTTTTCAAGT TTGGCATGGG CCAAACATCCA NANATCAACC TCGCCGGCCA CTGTGACCC	300
15	CGGAACAAACG GCTGCGCGCG CTTAACGAGC GAAATCCAGT CCTGCCAGGA GCGTGGAGTC	360
	AAGGTGATGC TCTCCATCGG AGGTGGCGGG TCTTATGGCC TGAGTTCCAC CGAANACGCC	420
	AAGGACGTGG CGTCATAACCT CTGGCACAGT TTCTTGGGTG GTTCTGCTGC TCGCTACTCT	480
20	CNACCCCTCG GGGATGCGGT TCTGGATGGC ATANACTTCA ACATCCCCGG AGGGAGCACA	540
	GAACACTATG ATGAACCTTG CGCTTCCCTC CNAGGGCTAC AACGAACAGG AAGCCGGAAC	600
25	CAAAAAAGTT TCACTTGAAT TGCTGCTCCC NCANTGTCC TTCCCCGATT ACTGGCTTTG	660
	GCAACCCACT CCAAAACAAA TNTCTCCNA CTTCCNTGTT GGGTTGCNA NTTCCNTTCC	720
	CAANCAAACC CCTTTCNNTT GC	742

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 794 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-U129

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

45	GGCACGAGGG CGTGGCGGAG ATGGGGAGCT GGCGGGCTCT GTTGCAGCGG CGGCTGCTGT	60
50	TGCTCTCTGC TTTGGCGGTG GCTGTTCTG TGAAGGCAGT CAGCANANAC NATTCCCCG	120
	CCGGCTTCAT TTTTGGCGCA GGCACCTCCG CTTATCAGGT ANAAGGTGCA GCTGCAGAGG	180
55	GGGAAANAAC ACCCAGCATT TGGGACACGT TTACGCATGC AGGGAGAACT TTGCACCAGA	240
	GCACCGGAGA CGTAGCAGCT GATCAGTATC ACAAGTACAA GGAAGATGTG AANCTGATGC	300
	ATGANATGGG CTTCGATGCT TACAGATTCT CCATCTCCTG GTCCANAGTT ATCCCCAATG	360
60	GTCGAGGGCC TGTGAATCCA CAAGGCTTGC GGTACTACAA CAACCTGATC GATGAGCTCN	420
	AAAGATATGG AATCCGAGCC TCATGTCACT CTTTACCACT TCGACCTTCC GCAAGCACTG	480
65	GAANACGAAT NCGCCGGGCA GCTGAACCCA AAGATCGTAN ANGACTTCAC CGCTTACGCC	540
	AACGTTTGC TTCANCNAAT TTGGGGATCN AATCTAGCAC TGGATCNCCC ATCAATGAAC	600
	CAACATANAT CCCGTCTCC GCCACNAATT CCGCATCTTC NCCCCGGCC CCTGCTCTT	660
70	ATCCCTTNCG CCTCCAACTG CNCCAAGGGC NACTCCCCCC CATTNTNAAN CCCATNNNNNT	720

CCNCCCCCCC CAATTAACCC NTTCTTGCTC TTCCCCCTTG CCTTCANCCA ACCCGCCCN	780
TTTCCNAAAA AANA	794

5 (2) INFORMATION FOR SEQ ID NO: 32:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 799 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- 15 (vii) IMMEDIATE SOURCE:
 (B) CLONE: U-U130

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

GGCACGAGCC GGCCTCAGGC ATATGGTGCG GTCGCTACAC GTGTTCAAGGC AAGGCCGGGA	60
GCCGGCCAGG ATCATCAGGG AAGCACTGTC GAAGGCGCTG GTGAAGTACT ACCCCCTTCGC	120
GGGGCGGTTG GTGGACNATC CCGAGGGCGG CGGCGAGGTT CGTGTGCTT GCACTGGCGA	180
GGGCCTTGG TTCGTCNAGG CCAAGGCGGA CTGCAGCTTG GAGGACGTGA AGTACCTCGA	240
TCTCCCGCTC ATGATCCCTG AGGACGCGCT CCTGCCAAG CCCTGCCCGG GACTGAACCC	300
CCTCGACCTC CCTCTCATGC TGCAGGTGAC ANANTTCGTG GGCGGCGGAT TCCTGGTCGG	360
CCTCATCTCC GTCCATACCA TCGCCGACGG CCTCGGCGTC NTCCANTTCA TCAACGCCGT	420
CGCCCGAAAT CGCCCGTGGC CTGCCNAANC CCACCGTGGA NCCTGCATGG TCCCGGGANG	480
TCNTACCCAA CCCACCTAAG CTGCCTCCCG GTGGCCCGCC CGTGTTCCTC CTCCCTCAAN	540
CTGCTCCACG CCACCGTCGA ACTATCCCT GACCACATCC ATCACGTCAA GTCCCCACAC	600
TTTGGANCTC ACCCGGCCAA CGCTGCTCTA CCTTCCACNT CCCCATCCCC AACCTGTTG	660
45 NAATCCCGCA CGCCCGCCN TCNACCTTGG AACCCAAGGC NTTCCAANC TTTGCAACCC	720
TTTTTTCCCTT TCCTTCCCCC CCCAAAANAA CTTCCCCCA CCCTTGTGTT TGNCNCCAAG	780
TTTTTTCCCTT CCTTGCCCC	799

50 (2) INFORMATION FOR SEQ ID NO: 33:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 759 base pairs
 (B) TYPE: nucleic acid
 55 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- 60 (vii) IMMEDIATE SOURCE:
 (B) CLONE: U-U43

65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

GGAGGTTGTT GTTCATGTCC CTACTTCGGG GTCTCCTGTA CAGATTGAAT TTCAAGTAAC	60
70 TAATAGCAGT GGCTACTTGG TGCTTCATTG GGGTGCAATT CATAATAGAA GGAATAACTG	120